



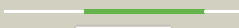


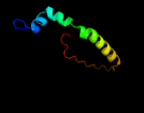

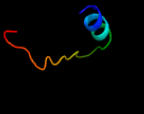
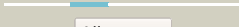



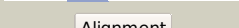

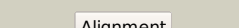
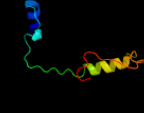
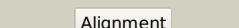
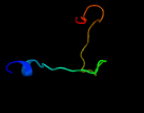
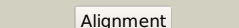



Phyre2

| | |
|---------------|------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD0690c_(-)_790027_791076 |
| Date | Fri Jul 26 01:50:26 BST 2019 |
| Unique Job ID | bf82b5d935eb3411 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|--|---|------------|--------|---|
| 1 | c5dplB_ |  Alignment |  | 72.9 | 17 | PDB header: transferase Chain: B; PDB Molecule: protein lysine methyltransferase 2; PDBTitle: the structure of pkmt2 from rickettsia typhi in complex with adohcy |
| 2 | c6cn0B_ |  Alignment |  | 70.0 | 17 | PDB header: transferase Chain: B; PDB Molecule: 16s rrna (guanine(1405)-n(7))-methyltransferase; PDBTitle: 2.95 angstrom crystal structure of 16s rrna methylase from proteus2 mirabilis |
| 3 | c5do0A_ |  Alignment |  | 56.4 | 18 | PDB header: transferase Chain: A; PDB Molecule: protein lysine methyltransferase 1; PDBTitle: the structure of pkmt1 from rickettsia prowazekii |
| 4 | c5mptA_ |  Alignment |  | 50.0 | 28 | PDB header: transferase Chain: A; PDB Molecule: citrinin polyketide synthase; PDBTitle: structure of the citrinin polyketide synthase cmet domain |
| 5 | d1af7a2 |  Alignment |  | 45.2 | 16 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Chemotaxis receptor methyltransferase CheR, C-terminal domain |
| 6 | c3tfwB_ |  Alignment |  | 30.7 | 18 | PDB header: transferase Chain: B; PDB Molecule: putative o-methyltransferase; PDBTitle: crystal structure of a putative o-methyltransferase from klebsiella2 pneumoniae |
| 7 | c3fzgA_ |  Alignment |  | 23.9 | 17 | PDB header: transferase Chain: A; PDB Molecule: 16s rrna methylase; PDBTitle: structure of the 16s rrna methylase arma |
| 8 | c5n5dA_ |  Alignment |  | 23.8 | 16 | PDB header: transferase Chain: A; PDB Molecule: methyltransferase; PDBTitle: crystal structure of the o-methyltransferase tomg from streptomyces2 achromogenes involved in tomaymycin synthesis in complex with sam |
| 9 | d1kyza2 |  Alignment |  | 22.9 | 19 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Plant O-methyltransferase, C-terminal domain |
| 10 | d1ogmx1 |  Alignment |  | 22.5 | 31 | Fold: Dextranase, N-terminal domain Superfamily: Dextranase, N-terminal domain Family: Dextranase, N-terminal domain |
| 11 | d1fyea_ |  Alignment |  | 22.0 | 25 | Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Aspartyl dipeptidase PepE |

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|----|-------------------------|-----------|--------------|------|----|--|
| 12 | d1qt1a_ | Alignment | | 21.9 | 20 | Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Xylose isomerase |
| 13 | c2yr0A_ | Alignment | | 21.5 | 13 | PDB header: transferase Chain: A: PDB Molecule: hypothetical protein ttha0223; PDBTitle: crystal structure of hypothetical methyltransferase ttha0223 from2 thermus thermophilus hb8 |
| 14 | c2ys9A_ | Alignment | | 20.1 | 23 | PDB header: transcription Chain: A: PDB Molecule: homeobox and leucine zipper protein homez; PDBTitle: structure of the third homeodomain from the human homeobox2 and leucine zipper protein, homez |
| 15 | c5xlxD_ | Alignment | | 19.1 | 15 | PDB header: transferase Chain: D: PDB Molecule: chemotaxis protein methyltransferase 1; PDBTitle: crystal structure of the c-terminal domain of cher1 containing sah |
| 16 | c3ssmB_ | Alignment | | 17.8 | 16 | PDB header: transferase Chain: B: PDB Molecule: methyltransferase; PDBTitle: myce methyltransferase from the mycinamycin biosynthetic pathway in2 complex with mg and sah, crystal form 1 |
| 17 | d2bm8a1 | Alignment | | 16.5 | 29 | Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Cmcl-like |
| 18 | c4azsA_ | Alignment | | 16.3 | 11 | PDB header: transferase Chain: A: PDB Molecule: methyltransferase wbdd; PDBTitle: high resolution (2.2 a) crystal structure of wbdd. |
| 19 | c5ufmB_ | Alignment | | 16.1 | 15 | PDB header: transferase Chain: B: PDB Molecule: methyltransferase domain protein; PDBTitle: crystal structure of burkholderia thailandensis 1,6-2 didemethyltoxoflavin-n1-methyltransferase with bound 1,6-3 didemethyltoxoflavin and s-adenosylhomocysteine |
| 20 | c2gslE_ | Alignment | | 15.2 | 12 | PDB header: structural genomics, unknown function Chain: E: PDB Molecule: hypothetical protein; PDBTitle: x-ray crystal structure of protein fn1578 from fusobacterium2 nucleatum. northeast structural genomics consortium target nr1. |
| 21 | c2r6zA_ | Alignment | not modelled | 14.3 | 16 | PDB header: transferase Chain: A: PDB Molecule: upf0341 protein in rsp 3' region; PDBTitle: crystal structure of the sam-dependent methyltransferase ngo1261 from2 neisseria gonorrhoeae, northeast structural genomics consortium3 target ngr48 |
| 22 | c4dnhA_ | Alignment | not modelled | 14.3 | 14 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of hypothetical protein smc04132 from sinorhizobium2 meliloti 1021 |
| 23 | d1u61a_ | Alignment | not modelled | 13.6 | 9 | Fold: RNase III domain-like Superfamily: RNase III domain-like Family: RNase III catalytic domain-like |
| 24 | c3tr6A_ | Alignment | not modelled | 13.4 | 14 | PDB header: transferase Chain: A: PDB Molecule: o-methyltransferase; PDBTitle: structure of a o-methyltransferase from coxiella burnetii |
| 25 | c6g4wq_ | Alignment | not modelled | 11.6 | 33 | PDB header: ribosome Chain: Q: PDB Molecule: 40s ribosomal protein s16; PDBTitle: cryo-em structure of a late human pre-40s ribosomal subunit - state a |
| 26 | d1j30a_ | Alignment | not modelled | 11.6 | 13 | Fold: Ferritin-like Superfamily: Ferritin-like Family: Ferritin |
| 27 | d1afra_ | Alignment | not modelled | 11.0 | 15 | Fold: Ferritin-like Superfamily: Ferritin-like Family: Ribonucleotide reductase-like |
| 28 | d1vpra1 | Alignment | not modelled | 10.9 | 35 | Fold: Lipocalins Superfamily: Lipocalins Family: Dinoflagellate luciferase repeat |

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|----|--------------------------|-----------|--------------|------|----|--|
| 29 | d1uxda_ | Alignment | not modelled | 10.6 | 13 | Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator |
| 30 | c5zy5B_ | Alignment | not modelled | 10.5 | 20 | PDB header: transferase Chain: B: PDB Molecule: probable catechol o-methyltransferase 1; PDBTitle: spcomt apo structure |
| 31 | c3icaB_ | Alignment | not modelled | 9.9 | 41 | PDB header: ligase Chain: B: PDB Molecule: phenylalanyl-trna synthetase beta chain; PDBTitle: the crystal structure of the beta subunit of a phenylalanyl-trna2 synthetase from porphyromonas gingivalis w83 |
| 32 | c3duwB_ | Alignment | not modelled | 9.7 | 19 | PDB header: transferase Chain: B: PDB Molecule: o-methyltransferase, putative; PDBTitle: crystal structural analysis of the o-methyltransferase from2 bacillus cereus in complex sah |
| 33 | c3l4gL_ | Alignment | not modelled | 9.6 | 45 | PDB header: ligase Chain: L: PDB Molecule: phenylalanyl-trna synthetase beta chain; PDBTitle: crystal structure of homo sapiens cytoplasmic phenylalanyl-trna2 synthetase |
| 34 | c4xalA_ | Alignment | not modelled | 9.4 | 27 | PDB header: viral protein Chain: A: PDB Molecule: tegument protein vp22; PDBTitle: crystal structure of the conserved core domain of vp22 from hsv-1 |
| 35 | c5w7kA_ | Alignment | not modelled | 9.0 | 17 | PDB header: transferase Chain: A: PDB Molecule: oxag; PDBTitle: crystal structure of oxag |
| 36 | d1sv0c_ | Alignment | not modelled | 8.3 | 17 | Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: Pointed domain |
| 37 | d1nda1_ | Alignment | not modelled | 8.2 | 18 | Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: Choline/Carnitine O-acyltransferase |
| 38 | d2d32a1_ | Alignment | not modelled | 7.9 | 15 | Fold: Glutamine synthetase/guanido kinase Superfamily: Glutamine synthetase/guanido kinase Family: Glutamate-cysteine ligase |
| 39 | c2qpxA_ | Alignment | not modelled | 7.4 | 19 | PDB header: hydrolase Chain: A: PDB Molecule: predicted metal-dependent hydrolase of the tim-barrel fold; PDBTitle: crystal structure of putative metal-dependent hydrolase (yp_805737.1)2 from lactobacillus casei atcc 334 at 1.40 a resolution |
| 40 | c3ig2B_ | Alignment | not modelled | 7.4 | 27 | PDB header: ligase Chain: B: PDB Molecule: phenylalanyl-trna synthetase beta chain; PDBTitle: the crystal structure of a putative phenylalanyl-trna synthetase2 (phers) beta chain domain from bacteroides fragilis to 2.1a |
| 41 | c6c8rA_ | Alignment | not modelled | 7.2 | 38 | PDB header: transferase Chain: A: PDB Molecule: loganic acid o-methyltransferase; PDBTitle: loganic acid o-methyltransferase complexed with sah and loganic acid |
| 42 | c2l8nA_ | Alignment | not modelled | 6.6 | 6 | PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional repressor cytr; PDBTitle: nmr structure of the cytidine repressor dna binding domain in presence2 of operator half-site dna |
| 43 | d1uxca_ | Alignment | not modelled | 6.6 | 13 | Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator |
| 44 | c3b5iB_ | Alignment | not modelled | 6.5 | 29 | PDB header: transferase Chain: B: PDB Molecule: s-adenosyl-l-methionine:salicylic acid carboxyl PDBTitle: crystal structure of indole-3-acetic acid methyltransferase |
| 45 | d1vg0a2_ | Alignment | not modelled | 6.4 | 29 | Fold: FAD-linked reductases, C-terminal domain Superfamily: FAD-linked reductases, C-terminal domain Family: GDI-like |
| 46 | c4azwA_ | Alignment | not modelled | 6.2 | 12 | PDB header: transferase Chain: A: PDB Molecule: wbdd; PDBTitle: crystal structure of monomeric wbdd. |
| 47 | d1hi9a_ | Alignment | not modelled | 6.2 | 17 | Fold: Dipeptide transport protein Superfamily: Dipeptide transport protein Family: Dipeptide transport protein |
| 48 | c2j5hA_ | Alignment | not modelled | 6.1 | 33 | PDB header: hormone/growth factor Chain: A: PDB Molecule: teratocarcinoma-derived growth factor; PDBTitle: nmr analysis of mouse cripto cfc domain |
| 49 | c4d0uD_ | Alignment | not modelled | 6.1 | 33 | PDB header: viral protein Chain: D: PDB Molecule: fiber protein; PDBTitle: crystal structure of the fiber head domain of the atadenovirus snake2 adenovirus 1, selenomethionine-derivative |
| 50 | c2lxrA_ | Alignment | not modelled | 5.8 | 38 | PDB header: oxidoreductase Chain: A: PDB Molecule: nadh dehydrogenase i subunit e; PDBTitle: solution structure of hp1264 from helicobacter pylori |
| 51 | d1jcb5_ | Alignment | not modelled | 5.7 | 41 | Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain |
| 52 | c4p8bA_ | Alignment | not modelled | 5.7 | 10 | PDB header: transport protein Chain: A: PDB Molecule: trap-type transporter, periplasmic component; PDBTitle: crystal structure of a trap periplasmic solute binding protein from2 ralstonia eutropha h16 (h16_a1328), target efi-510189, with bound3 (s)-2-hydroxy-2-methyl-3-oxobutanoate ((s)-2-acetolactate) |
| 53 | c4lfyB_ | Alignment | not modelled | 5.6 | 21 | PDB header: hydrolase Chain: B: PDB Molecule: dihydroorotase; PDBTitle: crystal structure of a dihydroorotase from burkholderia cenocepacia2 j2315 |
| 54 | c2kluA_ | Alignment | not modelled | 5.4 | 23 | PDB header: immune system, membrane protein Chain: A: PDB Molecule: t-cell surface glycoprotein cd4; |

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|----|-------------------------|-----------|--------------|-----|----|---|
| 54 | c2k0A_ | Alignment | not modelled | 5.4 | 53 | PDBTitle: nmr structure of the transmembrane and cytoplasmic domains2 of human cd4 PDB header: transferase |
| 55 | c3vptA_ | Alignment | not modelled | 5.4 | 19 | Chain: A: PDB Molecule: glutathione s-transferase sigma; PDBTitle: crystal structure of bombyx mori sigma-class glutathione transferase2 in apo form |
| 56 | c3r3hA_ | Alignment | not modelled | 5.3 | 19 | PDB header: transferase Chain: A: PDB Molecule: o-methyltransferase, sam-dependent; PDBTitle: crystal structure of o-methyltransferase from legionella pneumophila |
| 57 | d2gfqa1 | Alignment | not modelled | 5.3 | 46 | Fold: Phosphorylase/hydrolase-like Superfamily: AF0625-like Family: AF0625-like |
| 58 | c3wdkA_ | Alignment | not modelled | 5.3 | 18 | PDB header: ligase Chain: A: PDB Molecule: 4-phosphopantoate--beta-alanine ligase; PDBTitle: crystal structure of 4-phosphopantoate-beta-alanine ligase complexed2 with reaction intermediate |
| 59 | c3jzeC_ | Alignment | not modelled | 5.2 | 12 | PDB header: hydrolase Chain: C: PDB Molecule: dihydroorotase; PDBTitle: 1.8 angstrom resolution crystal structure of dihydroorotase (pyrc)2 from salmonella enterica subsp. enterica serovar typhimurium str. lt2 |
| 60 | c5zl6A_ | Alignment | not modelled | 5.1 | 5 | PDB header: isomerase Chain: A: PDB Molecule: histidine racemase; PDBTitle: histidine racemase from leuconostoc mesenteroides subsp. sake nbrc2 102480 |
| 61 | c3jwgA_ | Alignment | not modelled | 5.0 | 19 | PDB header: transferase Chain: A: PDB Molecule: methyltransferase type 12; PDBTitle: crystal structure analysis of the methyltransferase domain of2 bacterial-cthen1-c |